

SEQUENCE LISTING

<110> Tillett, D 5 Thomas, T

<120> A method of sequestering and/or purifying a polypeptide

10 <130> nuc2004

<140> 10/785,452

<141> 2004-02-25

<150> PCT/AU02/01159

<151> 2002-08-27

20 <160> 12

15

25

35

40

<210> 1

<211> 714

<212> DNA

<213> Aequorea victoria

30 <400> 1

atg agt aaa gga gaa ctt ttc act gga gtt gtc cca att ctt 45

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtt gaa tta gat ggc gat gtt aat ggg caa aaa ttc tct gtc agt

Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser
20 25 30

gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa

Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
35 40 45

ttt att tgc act act ggg aag cta cct gtt cca tgg cca aca ctt

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu 50 55 60

50

gtc act act ttc gcg tat ggt ctt caa tgc ttt gcg aga tac cca Val Thr Thr Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro gat cat atg aaa cag cat gac ttt ttc aag agt gcc atg ccc gaa Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu ggt tat gta cag gaa aga act ata ttt tac aaa gat gac ggg aac Gly Tyr Val Gln Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn tac aag aca cgt gct gaa gtc aag ttt gaa ggt gat acc ctt gtt Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val aat aga atc gag tta aaa ggt att gat ttt aaa gaa gat gga aac Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn att ctt gga cac aaa atg gaa tac aac tat aac tca cat aat gta Ile Leu Gly His Lys Met Glu Tyr Asn Tyr Asn Ser His Asn Val tac atc atg gca gac aaa cca aag aat gga atc aaa gtt aac ttc Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly Ile Lys Val Asn Phe aaa att aga cac aac att aaa gat gga agc gtt caa tta gca gac Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val Gln Leu Ala Asp cat tat caa caa aat act cca att ggc gat ggc cct gtc ctt tta His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu cca gac aac cat tac ctg tcc aca caa tct gcc ctt tcc aaa gat Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp

ccc aac gaa aag aga gat cac atg atc ctt ctt gag ttt gta aca Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val Thr gct gct ggg att aca cat ggc atg gat gaa cta tac aaa 714 Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys <210> 2 <211> 1149 <212> DNA <213> Escherichia coli <400>2atg ttt gaa cca atg gaa ctt acc aat gac gcg gtg att aaa gtc Met Phe Glu Pro Met Glu Leu Thr Asn Asp Ala Val Ile Lys Val atc ggc gtc ggc ggc ggc ggt aat gct gtt gaa cac atg gtg Ile Gly Val Gly Gly Gly Gly Asn Ala Val Glu His Met Val cgc gag cgc att gaa ggt gtt gaa ttc ttc gcg gta aat acc gat Arg Glu Arg Ile Glu Gly Val Glu Phe Phe Ala Val Asn Thr Asp gca caa gcg ctg cgt aaa aca gcg gtt gga cag acg att caa atc Ala Gln Ala Leu Arg Lys Thr Ala Val Gly Gln Thr Ile Gln Ile ggt agc ggt atc acc aaa gga ctg ggc gct ggc gct aat cca gaa Gly Ser Gly Ile Thr Lys Gly Leu Gly Ala Gly Ala Asn Pro Glu gtt ggc cgc aat gcg gct gat gag gat cgc gat gca ttg cgt gcg Val Gly Arg Asn Ala Ala Asp Glu Asp Arg Asp Ala Leu Arg Ala

```
gcg ctg gaa ggt gca gac atg gtc ttt att gct gcg ggt atg ggt
    315
    Ala Leu Glu Gly Ala Asp Met Val Phe Ile Ala Ala Gly Met Gly
                     95
                                                              105
5
    ggt ggt acc ggt aca ggt gcg gca cca gtc gtc gct gaa gtg gca
    360
    Gly Gly Thr Gly Thr Gly Ala Ala Pro Val Val Ala Glu Val Ala
                     110
                                         115
                                                              120
10
    aaa gat ttg ggt atc ctg acc gtt gct gtc gtc act aag cct ttc
    405
    Lys Asp Leu Gly Ile Leu Thr Val Ala Val Val Thr Lys Pro Phe
                     125
                                         130
                                                              135
15
    aac ttt gaa ggc aag aag cgt atg gca ttc gcg gag cag ggg atc
    450
    Asn Phe Glu Gly Lys Lys Arg Met Ala Phe Ala Glu Gln Gly Ile
                     140
                                         145
                                                              150
20
    act gaa ctg tcc aag cat gtg aac tct ctg atc act atc ccg aac
    495
    Thr Glu Leu Ser Lys His Val Asn Ser Leu Ile Thr Ile Pro Asn
                     155
                                         160
                                                              165
25
    gac aaa ctg ctg aaa gtt ctg ggc cgc ggt atc tcc ctg ctg gat
    540
    Asp Lys Leu Leu Lys Val Leu Gly Arg Gly Ile Ser Leu Leu Asp
                    170
                                         175
                                                              180
30
    gcg ttt ggc gca gcg aac gat gta ctg aaa ggc gct gtg caa ggt
   Ala Phe Gly Ala Ala Asn Asp Val Leu Lys Gly Ala Val Gln Gly
                    185
                                         190
                                                              195
35
    atc gct gaa ctg att act cgt ccg qgt ttg atg aac gtg gac ttt
    Ile Ala Glu Leu Ile Thr Arg Pro Gly Leu Met Asn Val Asp Phe
                    200
                                         205
                                                              210
40
    gca gac gta cgc acc gta atg tct gag atg ggc cac gca atg atg
    Ala Asp Val Arg Thr Val Met Ser Glu Met Gly His Ala Met Met
                    215
                                         220
                                                              225
45
    ggt tet gge gtg geg age ggt gaa gae egt geg gaa gaa get get
    720
    Gly Ser Gly Val Ala Ser Gly Glu Asp Arg Ala Glu Glu Ala Ala
                    230
                                         235
                                                              240
50
```

```
gaa atg gct atc tct tct ccg ctg ctg gaa gat atc gac ctg tct
    765
    Glu Met Ala Ile Ser Ser Pro Leu Leu Glu Asp Ile Asp Leu Ser
                                         250
                                                              255
5
    ggc gcg cgc ggc gtg ctg gtt aac atc acg gcg ggc ttc gac ctg
    810
    Gly Ala Arg Gly Val Leu Val Asn Ile Thr Ala Gly Phe Asp Leu
                                                              270
                    260
10
    cgt ctg gat gag ttc gaa acg gta ggt aac acc atc cgt gca ttt
    Arg Leu Asp Glu Phe Glu Thr Val Gly Asn Thr Ile Arg Ala Phe
                    275
                                         280
                                                              285
15
    gct tcc gac aac gcg act gtg gtt atc ggt act tct ctt gac ccg
    900
    Ala Ser Asp Asn Ala Thr Val Val Ile Gly Thr Ser Leu Asp Pro
                    290
                                         295
                                                              300
20
    gat atg aat gac gag ctg cgc gta acc gtt gtt gcg aca ggt atc
    945
    Asp Met Asn Asp Glu Leu Arg Val Thr Val Val Ala Thr Gly Ile
                    305
                                         310
                                                              315
25
    ggc atg gac aaa cgt cct gaa atc act ctg gtg acc aat aag cag
    990
    Gly Met Asp Lys Arg Pro Glu Ile Thr Leu Val Thr Asn Lys Gln
                    320
                                         325
                                                              330
30
    gtt cag cag cca gtg atg gat cgc tac cag cag cat ggg atg gct
    1035
    Val Gln Gln Pro Val Met Asp Arg Tyr Gln Gln His Gly Met Ala
                    335
                                         340
                                                              345
35
    ccg ctg acc caa gag cag aag ccg gtt gct aaa gtc gtg aat gac
    1080
    Pro Leu Thr Gln Glu Gln Lys Pro Val Ala Lys Val Val Asn Asp
                    350
                                         355
                                                              360
40
    aat gcg ccg caa act gcg aaa gag ccg gat tat ctg gat atc cca
    Asn Ala Pro Gln Thr Ala Lys Glu Pro Asp Tyr Leu Asp Ile Pro
                                         370
                    365
                                                              375
45
    gca ttc ctg cgt aag caa gct gat 1149
    Ala Phe Leu Arg Lys Gln Ala Asp
                    380
                                 383
```

<210> 3

<211> 546

5 <212> DNA

50

405

<213> Human rhinovirus

<400> 3 10 gga cca aac aca gaa ttt gca cta tcc ctg tta agg aaa aac ata Gly Pro Asn Thr Glu Phe Ala Leu Ser Leu Leu Arg Lys Asn Ile 10 15 15 atg act ata aca acc tca aag gga gag ttc aca ggg tta ggc ata Met Thr Ile Thr Thr Ser Lys Gly Glu Phe Thr Gly Leu Gly Ile 20 25 30 20 cat gat cgt gtc tgt gtg ata ccc aca cac gca cag cct ggt gat 135 His Asp Arg Val Cys Val Ile Pro Thr His Ala Gln Pro Gly Asp 35 40 25 gat gta cta gtg aat ggt cag aaa att aga gtt aag gat aag tac 180 Asp Val Leu Val Asn Gly Gln Lys Ile Arg Val Lys Asp Lys Tyr 50 aaa tta gta gat cca gag aac att aat cta gag ctt aca gtg ttg 30 225 Lys Leu Val Asp Pro Glu Asn Ile Asn Leu Glu Leu Thr Val Leu 65 75 35 act tta gat aga aat gaa aaa ttc aga gat atc agg gga ttt ata 270 Thr Leu Asp Arg Asn Glu Lys Phe Arg Asp Ile Arg Gly Phe Ile 85 90 40 tca gaa gat cta gaa ggt gtg gat gcc act ttg gta gta cat tca 315 Ser Glu Asp Leu Glu Gly Val Asp Ala Thr Leu Val Val His Ser 105 45 aat aac ttt acc aac act atc tta gaa gtt ggc cct gta aca atg 360 Asn Asn Phe Thr Asn Thr Ile Leu Glu Val Gly Pro Val Thr Met 115 110 120

gca gga ctt att aat ttg agt agc acc ccc act aac aga atg att

```
Ala Gly Leu Ile Asn Leu Ser Ser Thr Pro Thr Asn Arg Met Ile
                     125
                                          130
                                                               135
5
    cgt tat gat tat gca aca aaa act ggg cag tgt gga ggt gtg ctg
    450
    Arg Tyr Asp Tyr Ala Thr Lys Thr Gly Gln Cys Gly Gly Val Leu
                                                               150
10
    tgt gct act ggt aag atc ttt ggt att cat gtt ggc ggt aat gga
    Cys Ala Thr Gly Lys Ile Phe Gly Ile His Val Gly Gly Asn Gly
                     155
                                          160
                                                               165
15
    aga caa gga ttt tca gct caa ctt aaa aaa caa tat ttt gta gag
    540
    Arg Gln Gly Phe Ser Ala Gln Leu Lys Lys Gln Tyr Phe Val Glu
                     170
                                          175
                                                               180
20
    aaa caa 546
    Lys Gln
        182
25
    <210> 4
    <211> 27
30
    <212> DNA
    <213> artificial sequence
35
    <220>
    <223> Polymerase chain reaction oligonucleotide primer
    <400> 4
40
    atcatgagta aaggagaaga acttttc 27
    <210> 5
45
    <211> 29
    <212> DNA
50
    <213> artificial sequence
```

```
<220>
   <223> Polymerase chain reaction oligonucleotide primer
5
   <400> 5
    aggatcctta tttgtatagt tcatccatg 29
10
   <210> 6
   <211> 24
  <212> DNA
   <213> artificial sequence
   <220>
20
   <223> OTHER INFORMATION: Polymerase chain reaction
   oligonucleotide primer
   <400> 6
25
   ggcatatgtt tgaaccaatg gaac 24
   <210> 7
30
   <211> 27
   <212> DNA
35 <213> artificial sequence
   <220>
   <223> Polymerase chain reaction oligonucleotide primer
40
   <400> 7
    gtccatgggc ccttgaaata gtacttc 27
45
   <210> 8
   <211> 43
50
  <212> DNA
```

```
<213> artificial sequence
    <220>
   <223> Polymerase chain reaction oligonucleotide primer
    <400> 8
    gggcccttga aatagtactt ctagatcagc ttgcttacgc agg 43
10
    <210> 9
    <211> 27
15
    <212> DNA
    <213> artificial sequence
20
  <220>
    <223> Polymerase chain reaction oligonucleotide primer
    <400> 9
25
    cgccatggga ccaaacacag aatttgc 27
    <210> 10
30
    <211> 32
    <212> DNA
35 <213> artificial sequence
    <220>
    <223> Polymerase chain reaction oligonucleotide primer
40
    <400> 10
    gcggatccct attgtttctc tacaaaatat tg 32
45
    <210> 11
    <211> 24
   <212> DNA
50
```

```
<213> artificial sequence
   <220>
5 <223> Polymerase chain reaction oligonucleotide primer
   <400> 11
   ggcatatgtt tgaaccaatg gaac 24
10
   <210> 12
   <211> 25
15
   <212> DNA
   <213> artificial sequence
20
  <220>
   <223> Polymerase chain reaction oligonucleotide primer
   <400> 12
   cgccatggca gcttgcttac gcagg 25
25
```

30